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=> fil reg; d que l1

FILE 'REGISTRY' ENTERED AT 12:29:39 ON 26 MAY 2000
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STRUCTURE FILE UPDATES:   25 MAY 2000  HIGHEST RN 266695-80-1
DICTIONARY FILE UPDATES:  25 MAY 2000  HIGHEST RN 266695-80-1

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 11, 2000

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Structure search limits have been increased.  See HELP SLIMIT
for details.
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claim 18

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L1            49 SEA FILE=REGISTRY ABB=ON  C..C...C.{10-12}C...C..C/SQSP
```

. = any amine acid

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=> d rn cn l1 1-49; fil capl; s l1


L1   ANSWER 1 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   263557-86-4  REGISTRY
CN   Protein (Drosophila melanogaster gene Mst84Dc) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003672-derived protein GI 7298817

L1   ANSWER 2 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   263489-51-6  REGISTRY
CN   Protein (Drosophila melanogaster gene Mst84Dd) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003672-derived protein GI 7298818

L1   ANSWER 3 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   263489-50-5  REGISTRY
CN   Protein (Drosophila melanogaster gene Mst84Db) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003672-derived protein GI 7298816

L1   ANSWER 4 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   263484-91-9  REGISTRY
CN   Protein (Drosophila melanogaster gene BG:DS02740.19) (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   GenBank AE003650-derived protein GI 7298298

L1   ANSWER 5 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   263104-93-4  REGISTRY
CN   Protein (Drosophila melanogaster gene CG17666) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003540-derived protein GI 7294541

L1   ANSWER 6 OF 49  REGISTRY  COPYRIGHT 2000 ACS
RN   261150-58-7  REGISTRY
CN   RNA (avian leukosis-sarcoma virus strain AMV/AMAV minimal packaging signal
     M.psi.) (9CI)  (CA INDEX NAME)

L1   ANSWER 7 OF 49  REGISTRY  COPYRIGHT 2000 ACS
```

Searched by Barb O'Bryen

RN 260533-83-3 REGISTRY
CN DNA (human clone DNA59219-1613 protein PRO1359 cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 106: PN: WO0012708 FIGURE: 33 claimed protein
CN DNA (human clone DNA59219-1613 protein UNQ708 cDNA plus flanks)

L1 ANSWER 8 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 260348-99-0 REGISTRY
CN DNA (Naja naja naja clone pt7ZZ-NT neurotoxin cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (Chinese cobra venom clone pt7ZZ-NT short-chain neurotoxin cDNA plus flanks)

L1 ANSWER 9 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 255900-75-5 REGISTRY
CN 77: PN: US6018030 SEQID: 91 unclaimed protein (9CI) (CA INDEX NAME)

L1 ANSWER 10 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 255704-94-0 REGISTRY
CN DNA (synthetic Aequorea victoria green fluorescent protein) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: US6020192 SEQID: 3 claimed protein

L1 ANSWER 11 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 250242-56-9 REGISTRY
CN DNA (Drosophila melanogaster presenilin cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: US5986054 SEQID: 165 claimed protein

L1 ANSWER 12 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249906-26-1 REGISTRY
CN Protein (human bladder fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954460 SEQID: 357 claimed protein

L1 ANSWER 13 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249577-46-6 REGISTRY
CN DNA (Solanum tuberosum clone Ac64 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence

L1 ANSWER 14 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249577-44-4 REGISTRY
CN DNA (Solanum tuberosum clone Ac64 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence

L1 ANSWER 15 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249577-41-1 REGISTRY
CN DNA (Solanum tuberosum clone Ac15 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence

L1 ANSWER 16 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249577-36-4 REGISTRY

CN DNA (Solanum tuberosum clone 111h1 gene Rx protein cDNA) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN PN: WO9954490 FIGURE: 7A claimed sequence

L1 ANSWER 17 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249569-21-9 REGISTRY
CN PN: WO9954490 FIGURE: 7A unclaimed sequence (9CI) (CA INDEX NAME)

L1 ANSWER 18 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249569-19-5 REGISTRY
CN PN: WO9954490 FIG: 7A unclaimed protein (9CI) (CA INDEX NAME)

L1 ANSWER 19 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 249299-76-1 REGISTRY
CN PN: US5972684 SEQID: 3 unclaimed protein (9CI) (CA INDEX NAME)

L1 ANSWER 20 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 246852-79-9 REGISTRY
CN DNA (Mycobacterium tuberculosis antigen Ra12 fusion protein with Mycobacterium tuberculosis antigen TbH9 fusion protein with Mycobacterium tuberculosis antigen Ra35-specifying) (9CI) (CA INDEX NAME)

L1 ANSWER 21 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 234439-19-1 REGISTRY
CN DNA (human erythropoietin cDNA 5'-flank 224-nucleotide fragment) (9CI) (CA INDEX NAME)

L1 ANSWER 22 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 221220-54-8 REGISTRY
CN DNA (human 397-465-conductin-specifying cDNA) (9CI) (CA INDEX NAME)

L1 ANSWER 23 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 221111-80-4 REGISTRY
CN DNA (human nuclear receptor nNR2 cDNA) (9CI) (CA INDEX NAME)

L1 ANSWER 24 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 220140-39-6 REGISTRY
CN Protein (plasmid pPGH1 transposon Tn5502 open reading frame orf109) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF052749-derived protein GI 2995632
CN Protein (Pseudomonas putida strain H plasmid pPGH1 transposon Tn5502 open reading frame orf109)

L1 ANSWER 25 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 217945-23-8 REGISTRY
CN DNA (human clone HM74a G protein-coupled receptor cDNA plus flanks) (9CI) (CA INDEX NAME)

L1 ANSWER 26 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 209540-18-1 REGISTRY
CN DNA (gram-negative bacteria strain E-396 .beta.-carotene oxygenase gene crtZE396) (9CI) (CA INDEX NAME)

L1 ANSWER 27 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 209540-17-0 REGISTRY
CN DNA (gram-negative bacteria strain E-396 .beta.-carotene .beta.4-oxygenase gene crtWE396) (9CI) (CA INDEX NAME)

L1 ANSWER 28 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 201880-53-7 REGISTRY

CN Protein (Bacillus subtilis gene yhjQ) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank Y14081-derived protein GI 2226189
CN GenBank Z99109-derived protein GI 2633396
CN Protein (Bacillus subtilis strain 168 gene yhjQ)

L1 ANSWER 29 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 197981-22-9 REGISTRY
CN DNA (mouse strain B10.S H-2Dq gene 5'-regulatory region) (9CI) (CA INDEX NAME)

L1 ANSWER 30 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 188900-56-3 REGISTRY
CN DNA (Oryza sativa japonica strain Zhonghua-8 Bowman-Birk proteinase inhibitor gene RBBI plus flanks) (9CI) (CA INDEX NAME)

L1 ANSWER 31 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 185226-98-6 REGISTRY
CN Metallothionein 1 (Potamon potamios) (9CI) (CA INDEX NAME)

L1 ANSWER 32 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 185226-97-5 REGISTRY
CN Metallothionein 1a (Astacus astacus) (9CI) (CA INDEX NAME)

L1 ANSWER 33 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 171902-73-1 REGISTRY
CN Metallothionein II (Callinectes sapidus isoform IIb reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 34 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 171902-71-9 REGISTRY
CN Metallothionein II (Callinectes sapidus isoform IIa reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 35 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 171902-70-8 REGISTRY
CN Metallothionein I (Callinectes sapidus isoform Ib reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 36 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 171902-68-4 REGISTRY
CN Metallothionein I (Callinectes sapidus isoform Ia reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 37 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 157184-67-3 REGISTRY
CN 1-56-Metallothionein I (lobster) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1-56-Metallothionein 1 (lobster cadmium-binding domain-containing fragment)

L1 ANSWER 38 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 144905-11-3 REGISTRY
CN Protein (Drosophila melanogaster clone .lambda.Dm2.2 gene Mst84Dd reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 39 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 144905-09-9 REGISTRY
CN Protein (Drosophila melanogaster clone .lambda.Dm2.2 gene Mst84Dc reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 40 OF 49 REGISTRY COPYRIGHT 2000 ACS

RN 144905-07-7 REGISTRY
CN Protein (Drosophila melanogaster clone .lambda.Dm2.2 gene Mst84Db reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 41 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 114265-51-9 REGISTRY
CN Protein (Drosophila melanogaster gene mst(3)gl-9 reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AE003702-derived protein GI 7299816
CN Protein (Drosophila melanogaster gene Mst87F)

L1 ANSWER 42 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-67-6 REGISTRY
CN Protein (silkworm gene Hc-B.7 reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 43 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-60-9 REGISTRY
CN Protein (silkworm gene Hc-B.9 precursor reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 44 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-59-6 REGISTRY
CN Protein (silkworm gene Hc-B.7 precursor reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 45 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-55-2 REGISTRY
CN Protein (silkworm gene Hc-A.15 reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 46 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-53-0 REGISTRY
CN Protein (silkworm gene Hc-A.13 reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 47 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 104950-50-7 REGISTRY
CN Protein (silkworm gene Hc-A.8 reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 48 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 81458-84-6 REGISTRY
CN Metallothionein II (Scylla serrata protein moiety reduced) (9CI) (CA INDEX NAME)

L1 ANSWER 49 OF 49 REGISTRY COPYRIGHT 2000 ACS
RN 78213-76-0 REGISTRY
CN Metallothionein I (Scylla serrata protein moiety reduced) (9CI) (CA INDEX NAME)

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FILE COVERS 1967 - 26 May 2000 VOL 132 ISS 22
FILE LAST UPDATED: 25 May 2000 (20000525/ED)

Searched by Barb O'Bryen

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L2 30 L1

=> d ibib ab hitrn l2 1-30; fil hom

L2 ANSWER 1 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:246848 CAPLUS
DOCUMENT NUMBER: 132:289494
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; et al.
CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBast at

http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **114265-51-9**, Protein (Drosophila melanogaster gene mst(3)gl-9 reduced) **263484-91-9 263489-50-5 263489-51-6 263557-86-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L2 ANSWER 2 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:246831 CAPLUS
DOCUMENT NUMBER: 132:275066
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; et al.
CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **263104-93-4**

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L2 ANSWER 3 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:164617 CAPLUS
DOCUMENT NUMBER: 132:218003
TITLE: Nucleic acids encoding human membrane-bound proteins and receptors
INVENTOR(S): Baker, Kevin; Goddard, Audrey; Gurney, Austin L.; Smith, Victoria; Watanabe, Colin K.; Wood, William I.
PATENT ASSIGNEE(S): Genentech, Inc., USA
SOURCE: PCT Int. Appl., 773 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2000012708 | A2 | 20000309 | WO 1999-US20111 | 19990901 |

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

| | |
|---|---|
| US 1998-PV98716 | 19980901 |
| US 1998-PV98749 | 19980901 |
| US 1998-PV98750 | 19980901 |
| US 1998-PV98803 | 19980902 |
| US 1998-PV98821 | 19980902 |
| US 1998-PV98843 | 19980902 |
| US 1998-PV99536 | 19980909 |
| US 1998-PV99596 | 19980909 |
| US 1998-PV99598 | 19980909 |
| US 1998-PV99602 | 19980909 |
| US 1998-PV99642 | 19980909 |
| US 1998-PV99741 | 19980910 |
| US 1998-PV99754 | 19980910 |
| US 1998-PV99763 | 19980910 |
| US 1998-PV99792 | 19980910 |
| US 1998-PV99808 | 19980910 |
| US 1998-PV99812 | 19980910 |
| US 1998-PV99815 | 19980910 |
| US 1998-PV99816 | 19980910 |
| US 1998-PV100385 | 19980915 |

AB Membrane-bound proteins and receptor mols. have various industrial applications, including as pharmaceutical and diagnostic agents. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins. The present invention is directed to 123 novel polypeptides and to nucleic acid mols. encoding those polypeptides identified in human cDNA libraries by (1) extracellular domain homol. screening, (2) amylase screening, or (3) signal algorithm anal. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide mols. comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies

which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

IT **260533-83-3P**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(nucleotide sequence; nucleic acids encoding human membrane-bound proteins and receptors)

L2 ANSWER 4 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:78873 CAPLUS
DOCUMENT NUMBER: 132:133209
TITLE: Humanized green fluorescent protein genes with preferred codon usage for expression in mammalian cells
INVENTOR(S): Muzyczka, Nicholas; Zolotukhin, Sergei; Hauswirth, William
PATENT ASSIGNEE(S): University of Florida, USA
SOURCE: U.S., 70 pp., Cont.-in-part of U.S. Ser. No. 588,201.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| US 6020192 | A | 20000201 | US 1997-893327 | 19970716 |
| US 5874304 | A | 19990223 | US 1996-588201 | 19960118 |
| CA 2243088 | AA | 19970724 | CA 1997-2243088 | 19970117 |
| US 5968750 | A | 19991019 | US 1998-169605 | 19981009 |
| PRIORITY APPLN. INFO.: | | | US 1996-588201 | 19960118 |

AB Disclosed are synthetic and "humanized" versions of green fluorescent protein (GFP) genes adapted for high level expression in mammalian cells, esp. those of human origin. Base substitutions are made in various codons in order to change the codon usage to one more appropriate for expression in mammalian cells. Also provided are variant or mutant GFP gene sequences, and a sequence of GFP gene fused with a nuclear targeting sequence, SV40 large T-antigen nuclear localization signal. Recombinant adeno-assocd. virus (AAV) vectors carrying such humanized genes are also disclosed. In addn., various methods for using the efficient expression of humanized GFP in mammalian cells and in animals are described.

IT **255704-94-0**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; humanized green fluorescent protein genes with preferred codon usage for expression in mammalian cells)

REFERENCE COUNT: 11
REFERENCE(S):
(1) Anon; WO 9726333 1997 CAPLUS
(2) Carey; J Cell Biol 1996, V133(5), P985 CAPLUS
(3) Cubitt; TIBS 1995, V20, P448 CAPLUS
(5) Delagrave; Bio/Technology 1995, V13, P151 CAPLUS
(6) Goodman; Blood 1994, V84(5), P1492 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:67509 CAPLUS
DOCUMENT NUMBER: 132:119024
TITLE: Peptides comprising repetitive units of amino acids and DNA sequences encoding the same for production of fibers for use in prosthetics
INVENTOR(S): Ferrari, Franco A.; Richardson, Charles; Chambers,

James; Causey, Stuart; Pollock, Thomas J.; Cappello, Joseph; Crissman, John W.
PATENT ASSIGNEE(S): Protein Polymer Technologies, Inc., USA
SOURCE: U.S., 102 pp., Cont.-in-part of U.S. 5,641,648.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| US 6018030 | A | 20000125 | US 1995-482085 | 19950607 |
| US 5243038 | A | 19930907 | US 1987-114618 | 19871029 |
| JP 10014586 | A2 | 19980120 | JP 1997-63870 | 19871029 |
| JP 2000135092 | A2 | 20000516 | JP 1999-100595 | 19871029 |
| US 5641648 | A | 19970624 | US 1993-175155 | 19931229 |
| PRIORITY APPLN. INFO.: | | | US 1986-927258 | 19861104 |
| | | | US 1987-114618 | 19871029 |
| | | | US 1993-53049 | 19930422 |
| | | | US 1993-175155 | 19931229 |
| | | | JP 1988-500640 | 19871029 |
| | | | JP 1997-63870 | 19871029 |
| | | | US 1988-269429 | 19881109 |
| | | | US 1990-609716 | 19901106 |

AB Polypeptides comprising repetitive units of amino acids, as well as synthetic genes encoding the subject polypeptides are provided. The subject polypeptides are characterized by comprising repetitive units of amino acids, where the repetitive units are present in naturally occurring proteins, particularly naturally occurring structural proteins. The subject polypeptides find use in a variety of applications, such as structural components of prosthetic devices, synthetic fibers, and the like.

IT **255900-75-5**
RL: PRP (Properties)
(unclaimed protein sequence; peptides comprising repetitive units of amino acids and DNA sequences encoding the same for prodn. of fibers for use in prosthetics)

L2 ANSWER 6 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:4875 CAPLUS
DOCUMENT NUMBER: 132:218457
TITLE: Secondary structure analysis of a minimal avian leukosis-sarcoma virus packaging signal
AUTHOR(S): Banks, Jennifer D.; Linial, Maxine L.
CORPORATE SOURCE: Division of Basic Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA, 98109, USA
SOURCE: J. Virol. (2000), 74(1), 456-464
CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The authors previously identified a 160-nucleotide packaging signal, M.psi., from the 5' end of the Rous sarcoma virus genome. In this study, the authors det. the secondary structure of M.psi. by using phylogenetic anal. with computer modeling and heterologous packaging assays of point mutants. The results of the in vivo studies are in good agreement with the computer model. Addnl., the packaging studies indicate several structures which are important for efficient packaging, including a single-stranded bulge contg. the initiation codon for the short open reading frame, uORF3, as well as adjacent stem structures. Finally, the authors show that the L3 stem-loop at the 3' end of M.psi. is dispensable

for packaging, thus identifying an 82-nucleotide minimal packaging signal, .mu..psi., composed of the O3 stem-loop.

IT **261150-58-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ribonucleotide sequence; secondary structure anal. of minimal avian leukosis-sarcoma virus packaging signal)

REFERENCE COUNT: 25
REFERENCE(S):
(1) Aronoff, R; J Virol 1991, V65, P71 CAPLUS
(2) Banks, J; J Virol 1998, V72, P6190 CAPLUS
(3) Banks, J; J Virol 1999, V73, P8926 CAPLUS
(4) Banks, J; Semin Virol 1997, V8, P194 CAPLUS
(5) Berkowitz, R; Curr Top Microbiol Immunol 1996, V214, P177 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:733863 CAPLUS
DOCUMENT NUMBER: 131:347538
TITLE: Genetic sequences and proteins related to Alzheimer's disease
INVENTOR(S): St. George-Hyslop, Peter H.; Rommens, Johanna M.; Fraser, Paul E.
PATENT ASSIGNEE(S): The Hospital for Sick Children, HSC Research and Development Limited Partnership, Can.; The Governing Council of the University of Toronto
SOURCE: U.S., 131 pp., Cont.-in-part of U.S. Ser. No. 509,359.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| US 5986054 | A | 19991116 | US 1996-592541 | 19960126 |
| CA 2219214 | AA | 19961031 | CA 1996-2219214 | 19960429 |
| CN 1188508 | A | 19980722 | CN 1996-194902 | 19960429 |
| WO 9727296 | A1 | 19970731 | WO 1997-CA51 | 19970127 |
| W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG | | | | |
| AU 9712992 | A1 | 19970820 | AU 1997-12992 | 19970127 |
| EP 876483 | A1 | 19981111 | EP 1997-900531 | 19970127 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, LT, LV, FI, RO | | | | |
| US 6020143 | A | 20000201 | US 1997-888077 | 19970703 |
| US 5840540 | A | 19981124 | US 1997-967101 | 19971110 |
| PRIORITY APPLN. INFO.: | | | US 1995-431048 | 19950428 |
| | | | US 1995-496841 | 19950628 |
| | | | US 1995-509359 | 19950731 |
| | | | US 1996-592541 | 19960126 |
| | | | US 1996-21672 | 19960705 |
| | | | US 1996-21673 | 19960705 |
| | | | US 1996-21700 | 19960712 |
| | | | US 1996-29895 | 19961108 |
| | | | US 1997-34590 | 19970102 |

WO 1997-CA51 19970127

AB The present invention describes the identification, isolation and cloning of two human presenilin genes, PS-1 and PS-2, mutations in which lead to familial Alzheimer's disease. The Alzheimer's related membrane protein (ARMP) gene (or presenilin I (PSI)) gene was isolated, cloned and sequenced from within the AD3 region on chromosome 14q4.3. In addn., direct sequencing of RT-PCR products spanning this 3.0 kb cDNA transcript isolated from affected members of at least 8 large pedigrees linked to chromosome 14, has led to the discovery of missense mutations in each of these different pedigrees. These mutations are absent in normal chromosomes. Also identified are presenilin homolog genes in mice, Caenorhabditis elegans (SEL-12) and Drosophila melanogaster (DmPS). Transcripts and products of these genes are useful in detecting and diagnosing Alzheimer's disease, developing therapeutics for treatment of Alzheimer's disease, as well as the isolation and manuf. of the protein, and the constructions of transgenic animals expressing the mutant genes.

IT **250242-56-9P**
RL: ADV (Adverse effect, including toxicity); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(nucleotide sequence; genetic sequences and proteins related to Alzheimer's disease)

REFERENCE COUNT: 34
REFERENCE(S): (1) Anon; WO 91/19810 1991 CAPLUS
(5) Anon; WO 94/00569 1994 CAPLUS
(6) Anon; WO 94/10569 1994 CAPLUS
(7) Anon; WO 94/23049 1994 CAPLUS
(8) Anon; WO 97/03086 1997 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:691234 CAPLUS
DOCUMENT NUMBER: 131:333021
TITLE: Solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance
INVENTOR(S): Bendahmane, Abdelhafid; Baulcombe, David Charles; Kanyuka, Konstantin Valerievich
PATENT ASSIGNEE(S): Plant Bioscience Limited, UK
SOURCE: PCT Int. Appl., 124 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9954490 | A2 | 19991028 | WO 1999-GB1182 | 19990416 |
| WO 9954490 | A3 | 20000106 | | |
| W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| AU 9935296 | A1 | 19991108 | AU 1999-35296 | 19990416 |
| PRIORITY APPLN. INFO.: | | | GB 1998-8083 | 19980416 |
| | | | WO 1999-GB1182 | 19990416 |

AB Disclosed are nucleic acids encoding polypeptides which are capable of conferring extreme resistance (ER) against, and being triggered by, plant pathogens such as viruses (e.g. PVX and related isolates). Preferred nucleic acids encode the Rx polynucleotide from Solanum tuberosum , or a variety of homologues (naturally occurring or derivs.) thereof, such as 111h1; 221h2; Ac15; Ac64; K39.hom. Rx is a resistance gene from potato conferring extreme resistance against potato virus X. In addn. it gives resistance to Potex and Carlaviruses. It is able to induce cell death in some cells of leaves and thus lead to systemic acquired resistance against different pathogens. Rx genes are widely applicable in breeding programs because Rx is highly durable with only one natural isolate able to overcome the resistance and the resistance is extreme. Rx-mediated resistance is active in protoplasts where it suppresses viral replication or promotes degrdn. of viral RNA. Particular methods of activating resistance by using combinations of resistance gene and elicitor are also disclosed, which in certain cases lead to a hypersensitive response. This hypersensitive response is a secondary resistance response involving decoupled continuous activation of Rx by the 35S viral coat protein. Further aspects of the invention include specific primers, vectors, host cells, polypeptides, antibodies and transgenic plants, plus methods of producing and employing these, in particular for influencing a resistance trait in a plant.

IT **249577-36-4 249577-41-1 249577-44-4**
**249577-46-6**
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

IT **249569-19-5**, PN: WO9954490 FIG: 7A unclaimed protein
RL: PRP (Properties)
(unclaimed protein sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

IT **249569-21-9**
RL: PRP (Properties)
(unclaimed sequence; solanum tuberosum-derived viral resistance gene which induces cell death and extreme and hypervariable resistance)

L2 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:691206 CAPLUS
DOCUMENT NUMBER: 131:333014
TITLE: Human bladder nucleic acid sequences and proteins and their use in drug screening and bladder tumor inhibition
INVENTOR(S): Specht, Thomas; Hinzmann, Bernd; Schmitt, Armin; Pilarsky, Christian; Dahl, Edgar; Rosenthal, Andre
PATENT ASSIGNEE(S): Metagen Gesellschaft fur Genomforschung mbH, Germany
SOURCE: PCT Int. Appl., 355 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9954460 | A2 | 19991028 | WO 1999-DE1163 | 19990415 |
| W: JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| DE 19818620 | A1 | 19991028 | DE 1998-19818620 | 19980421 |

PRIORITY APPLN. INFO.: DE 1998-19818620 19980421

AB The invention relates to human nucleic acid sequences (mRNA, cDNA, genomic sequences) of normal bladder tissue, coding for proteins or parts thereof, in addn. to the use thereof. The invention also relates to the proteins that can be obtained according to said sequences and to the use thereof. Thus, through computer anal. of EST databanks and electronic Northern blotting, cDNAs characteristic of human bladder tissue were identified.

IT **249906-26-1P**, Protein (human bladder fragment)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human bladder nucleic acid sequences and proteins and their use in drug screening and bladder tumor inhibition)

L2 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:686627 CAPLUS
DOCUMENT NUMBER: 131:319671
TITLE: Cloning, expression, sequence and possible therapeutic use of human carbonic anhydrase VIII
INVENTOR(S): Bandman, Olga; Yue, Henry; Greenwald, Sara R.; Corley, Neil C.
PATENT ASSIGNEE(S): Incyte Pharmaceuticals, Inc., USA
SOURCE: U.S., 38 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| US 5972684 | A | 19991026 | US 1997-977767 | 19971125 |

AB The invention provides a human carbonic anhydrase isoform (CAVIII) and polynucleotides which identify and encode CAVIII. Nucleic acids encoding CAVIII were first identified in Incyte clone 2059155 from a cDNA library using a computer search for amino acid sequence alignments; a consensus sequence was derived from overlapping and/or extended nucleic acid sequences. Amino acid and cDNA sequences for CAVIII are reported. CAVIII is 328 amino acids in length. Expression of CAVIII has been shown and the enzyme activity has been demonstrated. Naturally occurring CAVIII has been purified using specific antibodies. The invention also provides expression vectors, host cells, agonists, antibodies and antagonists. The invention also provides methods for treating disorders assocd. with expression of CAVIII.

IT **249299-76-1**, PN: US5972684 SEQID: 3 unclaimed protein
RL: PRP (Properties)
(unclaimed protein sequence; cloning, expression, sequence and possible therapeutic use of human carbonic anhydrase VIII)

REFERENCE COUNT: 36
REFERENCE(S):
(6) Bergenhem, N; Int J Pept Protein Res 1989, V33, P140 CAPLUS
(7) Boren, K; Protein Sci 1996, V5, P2479 CAPLUS
(8) Briganti, F; Biochemistry 1997, V36, P10384 CAPLUS
(11) Centofanti, M; Pharmacol Res 1997, V35, P481 CAPLUS
(13) Cowen, M; J Clin Psychopharm 1997, V17, P190 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:685402 CAPLUS
DOCUMENT NUMBER: 132:204250

TITLE: Cloning and expression of a short-chain neurotoxin from Chinese cobra in Escherichia coli
AUTHOR(S): Cai, Qin; He, Zhi-Yong; Gong, Yi; Yang, Sheng-Li
CORPORATE SOURCE: Shanghai Research Center of Biotechnology, The Chinese Academy of Sciences, Shanghai, 200233, Peop. Rep. China
SOURCE: Yichuan (1999), 21(5), 1-4
CODEN: ICHUDW; ISSN: 0253-9772
PUBLISHER: Yichuan Zazhi Bianjibu
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A novel short-chain neurotoxin cDNA was cloned from Chinese cobra venom by RT-PCR. The cDNA was cloned into the pGEM-T vector and sequenced. It has a ORF encoding 83 amino acid residues and a 21 residues signal peptide. This neurotoxin gene of Chinese cobra was highly homogeneous to the short-chain neurotoxin gene of similar species reported in GenBank. Among the genes of neurotoxin from different species, the signal peptides were very conserved. The cDNA encoding the mature peptide was amplified by PCR and was cloned into pT7ZZ vector. The recombinant vector was transformed into Escherichia coli BL2(DE3). The E. coli highly expressed the fusion protein whose mol. wt. is 23kDa, after induced by 0.1 mol/L IPTG. The expressed protein was accumulated up to more than 25% of total bacterial protein.

IT **260348-99-0**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; cloning, cDNA sequence and recombinant expression of a short-chain neurotoxin from Chinese cobra)

L2 ANSWER 12 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:659510 CAPLUS
DOCUMENT NUMBER: 131:296204
TITLE: Fusion proteins of Mycobacterium tuberculosis antigens containing domains from more than one Mycobacterium protein and their uses
INVENTOR(S): Skeiky, Yasir A. W.; Alderson, Mark; Campos-Neto, Antonio
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 83 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9951748 | A2 | 19991014 | WO 1999-US7717 | 19990407 |
| WO 2000051748 | A3 | 20000203 | | |

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

| | | | | |
|---|---|---|---|---|
| AU 9934817 | A1 | 19991025 | AU 1999-34817 | 19990407 |
| PRIORITY APPLN. INFO.: | | | US 1998-56556 | 19980407 |
| | | | US 1998-223040 | 19981230 |
| | | | WO 1999-US7717 | 19990407 |

Searched by Barb O'Bryen

AB Fusion proteins contg. antigenic regions from two or more proteins (up to five) of Mycobacterium tuberculosis that can be used in the diagnosis, treatment and prevention of tuberculosis infection are described. These fusion proteins retain the antigenicity of the originals. A series of twelve fusion proteins contg. combinations of peptides from M. tuberculosis antigens were constructed by std. methods and manufd. as inclusion bodies in Escherichia coli. The fusion proteins stimulated T cell proliferation in PPD+ patients with proliferation patterns similar to those of the individual components. Immunization of mice with the fusion proteins induced strong interferon .gamma. and interleukin 4 responses with the strength of the responses depending upon the adjuvant used.

IT **246852-79-9**
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; fusion proteins of Mycobacterium tuberculosis antigens contg. domains from more than one Mycobacterium protein and their uses)

L2 ANSWER 13 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:495315 CAPLUS
DOCUMENT NUMBER: 131:139951
TITLE: Erythropoietin mutants with altered biological activity
INVENTOR(S): Sytkowski, Arthur J.; Grodberg, Jennifer
PATENT ASSIGNEE(S): Beth Israel Deaconess Medical Center, USA
SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9938890 | A1 | 19990805 | WO 1999-US2258 | 19990202 |
| W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| AU 9925766 | A1 | 19990816 | AU 1999-25766 | 19990202 |
| PRIORITY APPLN. INFO.: | | | US 1998-17631 | 19980203 |
| | | | WO 1999-US2258 | 19990202 |

AB The invention relates to DNA encoding modified, secretable erythropoietin proteins whose ability to regulate the growth and differentiation of red blood cell progenitors are different from the wild-type recombinant erythropoietin. The invention also relates to methods of modifying or altering the regulating activity of the secretable erythropoietin proteins and the use of the modified secretable erythropoietin proteins, for example, in in vivo therapeutics. Thus, oligonucleotide-directed mutagenesis was used to create mutant erythropoietin which resulted in substitution of amino acids at positions 100-109 within Domain 1. Arginine-103 was crit. for erythropoietin's biol. activity, and serine-104, leucine-105, and leucine-108 appear to play a role, as indicated by the decreased biol. activity of these mutants. Some of the mutant erythropoietin proteins demonstrated increased heat stability relative to the wild-type erythropoietin protein. Alterations in the noncoding regions of the erythropoietin gene can affect mRNA stability,

rates of translation, expression from host cells, protein processing, export from rough endoplasmic reticulum, extend and pattern of glycosylation, secretion dynamics and rate of export from the cell. The free energy for mRNA secondary structure for nucleotides 401-624 in the 5'-untranslated region of the erythropoietin gene is predicted to be -161.0 kcal/mol, and deletions in this area decrease the free energy values; similar changes in free energy are obsd for nucleotides 2773-2972 in the 3'-untranslated region. Erythropoietin mutants with modified biol. activities may be of use to treat anemia.

IT **234439-19-1**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(mutants in 5'- and 3'-UTR regions; erythropoietin mutants with altered biol. activity)

L2 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:189197 CAPLUS
DOCUMENT NUMBER: 130:232471
TITLE: The protein conductin and its application for diagnosis and gene therapy of colon cancer
INVENTOR(S): Behrens, Jurgen; Birchmeier, Walter
PATENT ASSIGNEE(S): Max-Delbruck-Centrum fur Molekulare Medizin, Germany
SOURCE: PCT Int. Appl., 22 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9911780 | A2 | 19990311 | WO 1998-DE2621 | 19980901 |
| WO 9911780 | A3 | 19990527 | | |
| W: CA, JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| DE 19840875 | A1 | 19990512 | DE 1998-19840875 | 19980901 |

PRIORITY APPLN. INFO.: DE 1997-19738205 19970902

AB The invention concerns the novel protein conductin that is able to regulate the .beta.-catenin function and interacts with the tumor suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon cancer. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations, variants and fragments of conductin with the corresponding coding genes and mRNA sequences are also included. Antibodies and nucleic acid probes for the detection of conductin are part of the diagnosis tools. For therapeutic purposes a vector contg. the conductin gene is constructed; substances that activate and reactivate conductin in the body are co-administered, e.g. a substance that activates the conductin promoter or stabilizes mRNA. The effect of conductin was proved using SW480 cells with APC mutation and thus increased .beta.-catenin level. Introduction of conductin resulted in the decrease of .beta.-catenin to the same concn. as in non APC mutated SW480 cells. In an expt. with Xenopus embryos it was shown that conductin inhibits the Wnt/Wingless signaling pathway via its interaction with .beta.-catenin.

IT **221220-54-8**
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; protein conductin and application for diagnosis

and gene therapy of colon cancer)

L2 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:166633 CAPLUS
DOCUMENT NUMBER: 130:219154
TITLE: DNA molecules encoding human nuclear receptor proteins
INVENTOR(S): Chen, Fang
PATENT ASSIGNEE(S): Merck & Co., Inc., USA
SOURCE: PCT Int. Appl., 82 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9910367 | A1 | 19990304 | WO 1998-US17826 | 19980827 |
| W: CA, JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| US 6054295 | A | 20000425 | US 1998-141000 | 19980826 |
| PRIORITY APPLN. INFO.: | | | US 1997-PV57090 | 19970827 |
| | | | US 1997-PV62902 | 19971021 |
| | | | US 1998-PV78633 | 19980319 |

AB The present invention discloses the isolation and characterization of cDNA mols. encoding two human nuclear receptor proteins, designated nNR1, nNR2 and/or nNR2-1. The nNR1 and nNR2 proteins share 95 and 77% homol. at the amino acid level to hERR2. The gene encoding nNR1 is located on locus 14q24.3-14q31, which is the Alzheimer disease gene 3 (AD3) locus. An alternative form of cDNA encoding nNR2 contains a 2-nucleotide insertion at nucleotide 1352, resulting in shifted reading frame and introduction of a TGA termination codon 33 nucleotides from the insertion site and thus a C-terminal truncated nNR2, nNR2-1. Also within the scope of the disclosure are recombinant vectors, recombinant host cells, methods of screening for modulators of nNR1, nNR2 and/or nNR2-1 activity, and prodn. of antibodies against nNR1, nNR2 and/or nNR2-1, or epitopes thereof.

IT **221111-80-4**, DNA (human nuclear receptor nNR2 cDNA)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; DNA mols. encoding human nuclear receptor proteins)

REFERENCE COUNT: 3
REFERENCE(S):
(1) Giguere, V; Nature 1998, V331(6151), P91
(2) Pettersson, K; Mechanisms of Development 1996, V54(2), P211 CAPLUS
(3) The Salk Institute For Biological Studies; WO 8803168 A1 1988 CAPLUS

L2 ANSWER 16 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1999:8025 CAPLUS
DOCUMENT NUMBER: 130:62689
TITLE: sequence and therapeutic applications for human Hm74a receptor isoform
INVENTOR(S): Elshourbagy, Nabil A.; Li, Xiaotong; Bergsma, Derk J.; Mooney, Jeffrey L.; Guerrera, Stephanie F.
PATENT ASSIGNEE(S): Smithkline Beecham Corporation, USA
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9856820 | A1 | 19981217 | WO 1998-US12386 | 19980612 |
| W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG | | | | |
| AU 9879660 | A1 | 19981230 | AU 1998-79660 | 19980612 |
| PRIORITY APPLN. INFO.: | | | US 1997-49480 | 19970612 |
| | | | WO 1998-US12386 | 19980612 |

AB HM74A polypeptides and polynucleotides and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing HM74A polypeptides and polynucleotides in therapy, and diagnostic assays for such. Therapeutic applications include treatment for bacterial or protozoan or fungal or viral infections. Specifically HIV-1, HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurol. mental disorders, anxiety , schizophrenia, manic depression, depression, delirium, dementia, severe mental retardation, dyskinesias, Huntingtons disease and Gilles dela Tourett's syndrome are treatable with this peptide.

IT **217945-23-8**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; sequence and therapeutic applications for human Hm74a receptor isoform)

REFERENCE COUNT: 2
REFERENCE(S):
(1) Devlin; Science 1990, V249, P404 CAPLUS
(2) Nomura; International Immunology 1993, V5(10), P1239 MEDLINE

L2 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:796616 CAPLUS
DOCUMENT NUMBER: 130:149395
TITLE: The transposable elements resident on the plasmids of Pseudomonas putida strain H, Tn5501 and Tn5502, are cryptic transposons of the Tn3 family
AUTHOR(S): Lauf, U.; Muller, C.; Herrmann, H.
CORPORATE SOURCE: Institut fur Genetik und Biochemie, Ernst-Moritz-Arndt-Universitat, Greifswald, D-17487, Germany
SOURCE: Mol. Gen. Genet. (1998), 259(6), 674-678
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Genes for (methyl)phenol degrdn. in Pseudomonas putida strain H (phl genes) are located on the plasmid pPGH1. Adjacent to the phl catabolic operon, a cryptic transposon, Tn5501, of the Tn3 family (class II transposons) was identified. The genes encoding the resolvase and the transposase are transcribed in the same direction, as is common for the Tn501 subfamily. The enzymes encoded by Tn5501, however, show only the overall homol. characteristic for resolvases/integrases and transposases of Tn3-type transposons. Therefore, it is likely that Tn5501 is not a

member of one of the previously defined subfamilies. Inactivation of the conditional lethal sacB gene was used to detect transposition of Tn5501. While screening for transposition events, another transposon was found integrated into sacB in one of the sucrose-resistant survivors. This element, Tn5502, is a composite transposon consisting of Tn5501 and an addnl. DNA fragment. It is flanked by inverted repeats identical to those of Tn5501 and the addnl. fragment is sepd. from the Tn5501 portion by an internal repeat (identical to the left terminal repeat). Transposition of phenol degrdn. genes could not be detected. Anal. of sequence data revealed that the phl genes are not located on a Tn5501-like transposon.

IT **220140-39-6**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; transposable elements resident on the plasmids of Pseudomonas putida strain H, Tn5501 and Tn5502, are cryptic transposons of the Tn3 family)

REFERENCE COUNT: 20
REFERENCE(S):
(1) Allmeier, H; Gene 1992, V111, P11 CAPLUS
(3) Gay, P; J Bacteriol 1985, V164, P918 CAPLUS
(4) Herrmann, H; FEMS Microbiol Lett 1987, V43, P133 CAPLUS
(5) Herrmann, H; Mol Gen Genet 1988, V214, P173 CAPLUS
(6) Herrmann, H; Mol Gen Genet 1995, V247, P240 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:394053 CAPLUS
DOCUMENT NUMBER: 129:94523
TITLE: Recombinant preparation of carotenoids using enzymes from Flavobacterium or gram-negative bacteria strain E-396 for feed or food industries
INVENTOR(S): Pasamontes, Luis; Tosigonkov, Juri
PATENT ASSIGNEE(S): F. Hoffmann-La Roche A.-G., Switz.
SOURCE: Jpn. Kokai Tokkyo Koho, 80 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| JP 10155497 | A2 | 19980616 | JP 1997-348653 | 19971202 |
| EP 872554 | A2 | 19981021 | EP 1997-120324 | 19971120 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| BR 9705676 | A | 19990525 | BR 1997-5676 | 19971201 |
| CN 1184159 | A | 19980610 | CN 1997-122604 | 19971202 |
| PRIORITY APPLN. INFO.: | | | EP 1996-810839 | 19961202 |

AB Disclosed is a method for industrial-scale prodn. of carotenoids by expression of the Flavobacterium strain R1534- or gram-neg. bacteria strain E-396-derived genes that are assocd. with the carotenoids-biosynthesis in a transgenic host such as Escherichia coli or Bacillus subtilis. The genes involved are crtE (for geranylgeranyl pyrophosphate synthetase), crtB (phytoene synthetase), crtI (phytoene desaturase), crtY (lycopene cyclase), all from Flavobacterium strain R1534, and crtZE396 (.beta.-carotene oxygenase) from gram-neg. bacteria strain E-396. Gene crtW encoding .beta.-carotene .beta.4-oxygenase of Alcaligenes strain PC-1 may also be used to improve the carotenoids prodn. Methods for fermn. prodn. of cantaxanthin, astaxanthin, adonixanthin, and zeaxanthin are claimed. Methods using genes crtEE396, crtBE396, crtIE396, crtYE396, crtZE396, and crtWE396, all from gram-neg. bacteria strain E-396, also

claimed. Use of carotenoids as food or feed additives is also claimed.

IT **209540-17-0 209540-18-1**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; recombinant prepn. of carotenoids using Flavobacterium or gram-neg. bacteria strain E-396 genes for feed or food industries)

L2 ANSWER 19 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1998:296873 CAPLUS
DOCUMENT NUMBER: 129:63855
TITLE: The 172 kb prkA-addAB region from 83.degree. to 97.degree. of the Bacillus subtilis chromosome contains several dysfunctional genes, the glyB marker, many genes encoding transporter proteins, and the ubiquitous hit gene
AUTHOR(S): Noback, Michiel A.; Holsappel, Siger; Kiewiet, Rense; Terpstra, Peter; Wambutt, Rolf; Wedler, Holger; Venema, Gerard; Bron, Sierd
CORPORATE SOURCE: Department of Genetics, Groningen Biomolecular Sciences and Biotechnology Institute (GBB), University of Groningen, Haren, 9751 NN, Neth.
SOURCE: Microbiology (Reading, U. K.) (1998), 144(4), 859-875
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 171812 bp nucleotide sequence between prkA and addAB (83.degree. to 97.degree.) on the genetic map of the Bacillus subtilis 168 chromosome was detd. and analyzed. An accurate phys./genetic map of this previously poorly described chromosomal region was constructed. One hundred and seventy open reading frames (ORFs) were identified on this DNA fragment. These include the previously described genes cspB, glpPFKD, spoVR, phoAIV, papQ, citRA, sspB, prsA, hpr, pbpF, hemEHY, aprE, comK and addAB. ORF yhaF in this region corresponds to the glyB marker. Among the striking features of this region are: an abundance of genes encoding (putative) transporter proteins, several dysfunctional genes, the ubiquitous hit gene, and five multidrug-resistance-like genes. These analyses have also revealed the existence of numerous paralogs of ORFs in this region: about two-thirds of the putative genes seem to have at least one paralogue in the B. subtilis genome.

IT **201880-53-7**, Protein (Bacillus subtilis gene yhjQ)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; of 172 kb prkA-addAB region from 83-97.degree. of Bacillus subtilis chromosome)

L2 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:748948 CAPLUS
DOCUMENT NUMBER: 128:150233
TITLE: The complete genome sequence of the gram-positive bacterium Bacillus subtilis
AUTHOR(S): Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Bertero, M. G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Borriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S. C.; Bron, S.; Brouillet, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N. M.; Choi, S.-K.; Codani, J.-J.; Connerton, I. F.; Cummings, N. J.; Daniel, R. A.; Denizot, F.; Devine, K. M.; Dusterhoft, A.; Ehrlich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.;

Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim, S.-Y.; Glaser, P.; Goffeau, A.; Golightly, E. J.; Grandi, G.; Guiseppi, G.; Guy, B. J.; Haga, K.; et al.
CORPORATE SOURCE: Unite de Biochemie Microbienne, Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Nature (London) (1997), 390(6657), 249-256
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Bacillus subtilis is the best-characterized member of the gram-pos. bacteria. Its genome of 4,214,810 base pairs comprises 4100 protein-coding genes. Of these protein-coding genes, 53% are represented once, while a quarter of the genome corresponds to several gene families that have been greatly expanded by gene duplication, the largest family contg. 77 putative ATP-binding transport proteins. In addn., a large proportion of the genetic capacity is devoted to the utilization of a variety of carbon sources, including many plant-derived mols. The identification of 5 signal peptidase genes, as well as several genes for components of the secretion app., is important given the capacity of Bacillus strains to secrete large amts. of industrially important enzymes. Many of the genes are involved in the synthesis of secondary metabolites, including antibiotics, that are more typically assocd. with Streptomyces species. The genome contains .gtoreq.10 prophages or remnants of prophages, indicating that bacteriophage infection has played an important evolutionary role in horizontal gene transfer, in particular in the propagation of bacterial pathogenesis.
IT **201880-53-7**, Protein (Bacillus subtilis gene yhjQ)
RL: PRP (Properties)
(amino acid sequence; complete genome sequence of Bacillus subtilis)

L2 ANSWER 21 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:634275 CAPLUS
DOCUMENT NUMBER: 127:327167
TITLE: Conservation of the H-2 BF1 binding motif 5' of the H-2Ds, Ks and Dq genes
AUTHOR(S): Brown, G. D.; Morris, D. R.; Meruelo, D.
CORPORATE SOURCE: Department of Pathology and Kaplan Cancer Centre, New York University Medical Centre, New York, NY, USA
SOURCE: Eur. J. Immunogenet. (1997), 24(4), 241-257
CODEN: EJOIE3; ISSN: 0960-7420
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The biol. consequences of radiation leukemia virus (RadLV) infection include the stimulation of H-2 antigen expression soon after injection of the virus. Early studies demonstrated that resistance to RadLV-induced leukemia in certain mouse strains is mediated by genes in the H-2D region of the major histocompatibility complex (MHC). Recent studies have shown that elevated H-2D regions of the major histocompatibility complex (MHC). Recent studies have shown that elevated H-2Dd expression on the thymocyte cell surface of resistant mouse strains results from increased mRNA transcription and is correlated with elevated levels of a DNA-binding activity that recognizes a short DNA sequence 5' of the start of transcription for the H-2Dd gene. This binding activity has been termed H-2 binding factor 1 (H-2 BF1) and is found exclusively in the thymus. In an effort to examinethe H-2 genes of RadLV-susceptible mice for the presence of the H-2 BF1 binding target, we have clones class I genes from the highly susceptible B10.S mouse strain and have identified both the Ds and the Ks genes. The entire genomic sequence for the Ds gene has been detd. and is reported here. In addn., the 5' regulatory region of the

previously cloned Dq gene has been sequenced; mice of the Dq haplotype are also susceptible to RadLV-induced leukemia. In this report, we show that the H-2 BF1 DNA binding sequence is present 5' of each of these three class I genes.

IT **197981-22-9**
RL: PRP (Properties)
(nucleotide sequence; conservation of the H-2 BF1 binding motif 5' of the H-2Ds, Ks and Dq genes)

L2 ANSWER 22 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1997:212344 CAPLUS
DOCUMENT NUMBER: 126:273049
TITLE: Molecular cloning and sequence analysis of a gene encoding rice proteinase inhibitor
AUTHOR(S): Xie, Ming; Chen, Xin; Qu, Lijia; Liu, Hong; Gu, Hongya; Chen, Zhanliang
CORPORATE SOURCE: State Key Lab. Protein Engineering & Plant Genetic Engineering, Beijing Univ., Beijing, 100871, Peop. Rep. China
SOURCE: Zhiwu Xuebao (1996), 38(6), 444-450
CODEN: CHWHAY; ISSN: 0577-7496
PUBLISHER: Kexue
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB With the primers designed basing on the terminal amino acid sequences of rice proteinase inhibitor and the preferred codons of rice genes, a new gene coding for a rice proteinase inhibitor was amplified and cloned from Oryza sativa var. japonica (cv. Zhonghua 8) using PCR technique. The gene contains 408 base-pairs and encodes 133 amino acid residues. The deduced amino acid sequence showed duplicated Bowman-Birk type structure and active sites specific to trypsin, and it has relatively high homol. with those of proteinase inhibitors from wheat and bean. The new gene (RBBI) shares 74.8% homol. with a rice bran trypsin inhibitor reported previously. The evolutionary characteristics of the proteinase inhibitor family was also discussed.

IT **188900-56-3**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; cloning and sequencing of rice Bowman-Birk proteinase inhibitor gene RBBI)

L2 ANSWER 23 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1996:726575 CAPLUS
DOCUMENT NUMBER: 126:56496
TITLE: Primary structures of decapod crustacean metallothioneins with special emphasis on freshwater and semi-terrestrial species
AUTHOR(S): Pedersen, Soeren N.; Pedersen, Knud L.; Hoejrup, Peter; Depledge, Michael H.; Knudsen, Jens
CORPORATE SOURCE: Inst. Biol., Odense Univ., Odense, DK-5230, Den.
SOURCE: Biochem. J. (1996), 319(3), 999-1003
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Cadmium injections induced only a single form of metallothionein (MT) in the midgut gland of Potamon potamios, whereas the same treatment induced two isoforms in Astacus astacus. The only difference between the two latter isoforms was that one had an extra N-terminal methionine residue. MT from P. potamios showed structural differences from other decapod crustacean MTs. It contained a Gly-Thr motif at positions 8 and 8a, which had previously been found only in certain vertebrate and molluscan MTs.

Furthermore, P. potamios MT contained two to three times as many glutamic acid residues as normally found in decapod crustacean MT. The primary structure of MT from the freshwater crayfish A. astacus showed a high degree of sequence identity with MT from other decapod crustaceans, esp. the marine astacidean Homarus americanus; although, two valine residues were unexpectedly found at positions 8 and 21, where lysine residues are normally found.

IT **185226-97-5**, Metallothionein 1a (Astacus astacus)
**185226-98-6**, Metallothionein 1 (Potamon potamios)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of; primary structures of freshwater (Astacus astacus) and semi-terrestrial (Potamon potamios) decapod crustacean metallothioneins)

L2 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1995:883450 CAPLUS
DOCUMENT NUMBER: 124:48559
TITLE: Primary structure and tissue-specific expression of blue crab (Callinectes sapidus) metallothionein isoforms
AUTHOR(S): Brouwer, Marius; Enghild, Jan; Hoexum-Brouwer, Thea; Thogersen, Ida; Truncali, Andrea
CORPORATE SOURCE: Marine Biomedical Center, Duke Univ. Sch. Environment Marine Lab., Beaufort, NC, 28516, USA
SOURCE: Biochem. J. (1995), 311(2), 617-22
CODEN: BIJOAK; ISSN: 0264-6021
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In aquatic animals, synthesis of the metal-binding protein metallothionein (MT) can be induced through exposure to elevated levels of metals in food or water. Whether the different routes of exposure lead to expression of different metallothionein isoforms in different tissues is unknown. In this study the authors examd. the induction of metallothionein isoforms in the hepatopancreas and gills of the blue crab Callinectes sapidus. When blue crabs are exposed to cadmium in their diet, the metal accumulates in the hepatopancreas. Size-exclusion and anion-exchange chromatog. show the presence of five low-mol.-mass cadmium-binding proteins. All of the obsd. cadmium-binding proteins belong to the class I MT family. They are designated as MT-Ia, MT-Ib, MT-Ic, MT-IIa and MT-IIb. All purified proteins run as single peaks upon rechromatog. on anion-exchange HPLC, except for MT-Ic, which segregates into two peaks corresponding to MT-Ia and MT-Ic. The amino acid sequence of MT-Ia and MT-Ic is identical. MT-Ib differs from MT-Ia and MT-Ic only in having an extra N-terminal methionine. The 18 cysteine residues in MT-Ia and MT-IIa occur in identical positions; however, of the remaining 40 amino acids, 15 are different. MT-IIb is identical with MT-IIa, except for an extra methionine residue at its N-terminal position. It appears therefore that, of the five obsd. CdMTs, only two are the products of distinct genes. CdMT-Ia and -IIa are post-translationally modified forms of Ib and IIb, resp., and CdMT-Ia and -Ic appear to be conformational isomers. Cadmium-induced expression of the two genes is tissue-specific. When crabs are exposed to cadmium in the water, the metal accumulates in the gills, where it is bound to MT-II. MT-I is virtually absent.

IT **171902-68-4 171902-70-8 171902-71-9**
**171902-73-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; primary structure and tissue-specific expression of blue crab (Callinectes sapidus) metallothionein isoforms)

L2 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1994:528180 CAPLUS
DOCUMENT NUMBER: 121:128180
TITLE: Sequential Proton Resonance Assignments and Metal Cluster Topology of Lobster Metallothionein-1
AUTHOR(S): Zhu, Zhiwu; DeRose, Eugene F.; Mullen, Gregory P.; Petering, David H.; Shaw, C. Frank, III
CORPORATE SOURCE: Department of Chemistry, University of Wisconsin, Milwaukee, WI, 53211, USA
SOURCE: Biochemistry (1994), 33(30), 8858-65
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English

AB NMR studies of 111Cd6-MT 1 from lobster have been conducted to det. coordination structure of Cd-thiolate binding in the protein. Sequential proton resonance assignments were made using std. two-dimensional 1H NMR methods. Two-dimensional 1H-111Cd HMQC expts. were then carried out to det. the cadmium-cysteine connectivities in the protein. With this information, it was established that the six Cd ions exist in two different Cd3S9 clusters, each involving three bridging and six terminal thiolate ligands. Sequential cysteines in the sequence provide the sulfhydralligands for each cluster and do not overlap, as has been found in mammalian metallothionein. Comparison of the N-terminal, Cd3S9 B-type cluster of lobster MT 1 with the Cd3S9 cluster from rabbit MT 2 shows that while eight of the nine cysteine residues occupy homologous positions in their sequences, three of the 12 Cd-thiolate connectivities are different. Similarly, the C-terminal B-cluster of lobster MT 1 was compared with the Cd4S11 cluster of mammalian MT 2, excluding the two terminal cysteine sulfhydryl groups that convert this cluster from A- to B-type. As above, eight of nine cysteine positions are identical, yet five of 12 Cd-sulfhydryl connections are different. These differences are expanded when the role of each cysteine as bridging or terminal ligands in the clusters is considered.

IT **157184-67-3**
RL: RCT (Reactant)
(cadmium coordination by, NMR study of)

L2 ANSWER 26 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1993:1730 CAPLUS
DOCUMENT NUMBER: 118:1730
TITLE: A cluster of four genes selectively expressed in the male germ line of Drosophila melanogaster
AUTHOR(S): Kuhn, Rainer; Kuhn, Claudia; Boersch, Dagmar; Glaetzer, Karl Heinz; Schaefer, Ulrich; Schaefer, Mireille
CORPORATE SOURCE: Inst. Genet., Heinrich-Heine-Univ., Duesseldorf, 4000/1, Germany
SOURCE: Mech. Dev. (1991), 35(2), 143-51
CODEN: MEDVE6; ISSN: 0925-4773
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gene Mst87F is exclusively expressed in the male germ line and is subject to translational regulation. The Mst87F mRNA is transcribed in the primary spermatocytes, stored for 3 days and then subsequently translated in the post-elongation period of spermiogenesis. Here the isolation of a cluster of 4 small genes closely related in structure and function to Mst87F is reported. These genes are located at polytene band 84D on the right arm of chromosome and are named Mst84Da, Mst84Db, Mst84Dc and Mst84Dd. All 4 genes encode putative proteins composed primarily of a repetitive motif of cysteine-glycine-proline. The genes are exclusively expressed in the male germ line. The poly(A) tail of the Mst84D mRNAs increases in length at day 3 of pupal development, the time at which a similar change in Mst87F mRNA and translation has been shown to begin. In

addn. a conserved 12 base pair element was identified within the 5' untranslated region (UTR) of each gene which is also found at an identical position in Mst87F and which has been demonstrated to be the structural element for translational control of Mst87F expression (Schaefer, U., et al., 1990). The gene cluster was mapped to a small deletion assocd. with a rotund mutation at 84D. Although flies with a homozygous deletion of the cluster still produce motile sperm, electron microscopic examn. revealed numerous malformations in the ultrastructure of the axoneme resulting in a drastic redn. of motile sperm.

IT **144905-07-7**, Protein (Drosophila melanogaster gene Mst84Db reduced) **144905-09-9**, Protein (Drosophila melanogaster gene Mst84Dc reduced) **144905-11-3**, Protein (Drosophila melanogaster gene Mst84Dd reduced)
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L2 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1988:449380 CAPLUS
DOCUMENT NUMBER: 109:49380
TITLE: Cis-acting regions sufficient for spermatocyte-specific transcriptional and spermatid-specific translational control of the Drosophila melanogaster gene mst(3)gl-9
AUTHOR(S): Kuhn, Rainer; Schaefer, Ulrich; Schaefer, Mireille
CORPORATE SOURCE: Inst. Genet., Univ. Duesseldorf, Duesseldorf, D-4000, Fed. Rep. Ger.
SOURCE: EMBO J. (1988), 7(2), 447-54
CODEN: EMJODG; ISSN: 0261-4189
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In Drosophila spermatogenesis, transcription occurs only premeiotically while translation can be detected also in postmeiotic spermatids. To analyze the underlying processes, mst(3)gl-9, a gene specifically expressed in the male germ cells of D. melanogaster, was studied. The putative protein encoded by mst(3)gl-9 is mostly composed of repetitive Cys-Gly-Pro motifs. The transcriptional and translational control of expression of mst(3)gl-9 was investigated by P-mediated transformation. Only 102 bp of 5' upstream sequences and the first 201 bp of the gene are sufficient to maintain the gene-specific characteristics of expression, namely premeiotic transcription and postmeiotic translation sepd. by 3 days of development.

IT **114265-51-9**, Protein (Drosophila melanogaster gene mst(3)gl-9 reduced)
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 28 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1986:585048 CAPLUS
DOCUMENT NUMBER: 105:185048
TITLE: The silkmoth late chorion locus. I. Variation within two paired multigene families
AUTHOR(S): Burke, William D.; Eickbush, Thomas H.
CORPORATE SOURCE: Dep. Biol., Univ. Rochester, Rochester, NY, 14627, USA
SOURCE: J. Mol. Biol. (1986), 190(3), 343-56
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The 140 .times. 103 base late chorion locus of B. mori contains two 15-member multigene families arranged in tightly linked pairs, which are divergently transcribed (the high-cysteine A (HcA) and the high-cysteine B (HcB) families). Previous DNA hybridization expts. have indicated that

all members of these gene families contain a complex pattern of shared sequence variation. The sequence anal. in this paper involving all 15 gene pairs allows a comprehensive examn. of the nature of this variation. Av. sequence homol. between gene pairs is: 95% for the protein-encoding regions; 93% for the common 272-base-pair 5' flanking region; 87% for the introns; and 88% for the 3' untranslated regions. Considering the great degree of sequence homol. in the coding regions, an unexpectedly high level of variation is found in the deduced protein sequences. Over 50% of the nucleotide substitutions in the protein-encoding regions lead to amino acid replacements, most of which involve a change in charge or effect the secondary structure of the protein. In addn., significant differences in length between the proteins occur in the C-terminal arm. In both families, the major portion of this arm is composed of Cys-Gly-Gly and Cys-Gly subrepeats forming a (Cys-Gly-Gly)2-(Cys-Gly)2 major repeat. Differences in the no. of complete and partial repeats results in deduced protein sequences that contain arms varying from 32 to 54 amino acid residues for members of the HcA family and 14 to 88 residues for the HcB family. The high level of variation in protein compn. indicates a lack of strong selective pressure. The high level of DNA sequence homol. maintained by these genes in the coding as well as in the noncoding regions is apparently the result of sequence exchange between family members.

IT **104950-50-7 104950-53-0 104950-55-2**
**104950-59-6 104950-60-9 104950-67-6**
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 29 OF 30 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1982:157702 CAPLUS
DOCUMENT NUMBER: 96:157702
TITLE: Crab metallothionein. Primary structures of metallothioneins 1 and 2
AUTHOR(S): Lerch, Konrad; Ammer, Doris; Olafson, Robert W.
CORPORATE SOURCE: Biochem. Inst., Univ. Zurich, Zurich, CH-8028, Switz.
SOURCE: J. Biol. Chem. (1982), 257(5), 2420-6
CODEN: JBCHA3; ISSN: 0021-9258
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AB The complete amino acid sequences of metallothionenins 1 and 2 from the crab Scylla serrata are reported. The primary structures were detd. by automated and manual sequence anal. on fragments produced by cleavage of the S-pyridylethylated, S-aminoethylated, and S-carbamidomethylated proteins with trypsin. The 2 isoproteins consist of 58 and 57 amino acid residues, resp., and show a sequence identity of 83%. Comparison of their primary structures with the known sequences of 3 representative mammalian metallothioneins and Neurospora Cu-metallothionein reveals a high degree of sequence homol. among the 6 proteins. The abundant cysteinyl residues were strongly conserved, in agreement with their function as metal ligands.

IT **78213-76-0 81458-84-6**
RL: PRP (Properties)
(amino acid sequence of)

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TITLE: Amino acid sequence of crab metallothionein
AUTHOR(S): Lerch, K.; Ammer, D.; Olafson, R. W.
CORPORATE SOURCE: Biochem. Inst., Univ. Zurich, Zurich, CH-8028, Switz.
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AB The amino acid sequence of metallothionein (I) isoprotein MT-1 from the crab, Scylla serrata, is reported and compared with the primary structures of human and mouse I and of Cu-I of Neurospora crassa. Crab I contained 58 amino acids, only slightly smaller than the value of 61 typically found for sequenced mammalian I. In contrast to the vertebrate I proteins sequenced so far, crab I displayed a free N-terminus. There were a smaller no. of cysteine residues (18) in crab I vs. 20 in the mammalian forms. The spatial distribution of these cysteine residues, the principal metal-binding ligands in I, was also preserved in crab I; 5 Cys-X-Cys sequences in crab I vs. 7 Cys-X-Cys sequences in mammalian I. A comparison of aligned residues of crab I MT-1 with human MT-2 showed 46% identity in sequence and 48% homol. on considering arginine as a conservative replacement for lysine. There was a rigid sequence conservation between residues 21-31, suggesting a fundamental structure-function importance to this stretch. In contrast, the amino acid sequence of Neurospora I was highly altered in this region which may be related to the fact that Neurospora I binds Cu.

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RL: PRP (Properties)
(amino acid sequence of)

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